

QY 1561 GATCGTGTGTTGAAAAAGGGGACTTGGTATTTGTGTGTTCAACTTCCACTGGAGTAATAGCTA 1620
Db 1561 GATCGTGTGTTGAAAAAGGGGACTTGGTATTTGTGTGTTCAACTTCCACTGGAGTAATAGCTA 1620
QY 1621 TTTCGACTACCGGGTGTGTTTAAAGCCTGGGAAGTACAAAGTTGTCTTAGACTCAGA 1680
Db 1621 TTTCGACTACCGGGTGTGTTTAAAGCCTGGGAAGTACAAAGTTGTCTTAGACTCAGA 1680
QY 1681 CGCCGGGACTCTTTGGTGGATTTGGTAGGATCCATCAGACTGCAGAGCACTTCACTTCTGA 1740
Db 1681 CGCCGGGACTCTTTGGTGGATTTGGTAGGATCCATCAGACTGCAGAGCACTTCACTTCTGA 1740
QY 1741 CTGCCAATCATGACAAACAGGCCCATTCGTTCTCAGTGTACACTCCTAGCAGAACCTGTGT 1800
Db 1741 CTGCCAATCATGACAAACAGGCCCATTCGTTCTCAGTGTACACTCCTAGCAGAACCTGTGT 1800
QY 1801 TGTCTATGCTCCCAATGAACATAACAGCAAAAGTGCAGCATACGATGCACGCTGTGTTC 1860
Db 1801 TGTCTATGCTCCCAATGAACATAACAGCAAAAGTGCAGCATACGATGCACGCTGTGTTC 1860
QY 1861 TAGCACTAGCAAGAAAAATCGTATGTTCAATACACCAAGGTGCAAGTTTAAATAAGGGT 1920
Db 1861 TAGCACTAGCAAGAAAAATCGTATGTTCAATACACCAAGGTGCAAGTTTAAATAAGGGT 1920
QY 1921 TTGCTTCAACGAGTCTGATAGACAAAGCAACATGATGATGTCTGTCTGTCTCCCAAT 1980
Db 1921 TTGCTTCAACGAGTCTGATAGACAAAGCAACATGATGATGTCTGTCTGTCTCCCAAT 1980
QY 1981 TCCAGGGCGTGTGGAGAAAAATGCTCATCTGTGTATTTTATGGATCAGGAGGAAA 2040
Db 1981 TCCAGGGCGTGTGGAGAAAAATGCTCATCTGTGTATTTTATGGATCAGGAGGAAA 2040
QY 2041 CCTCCCCCAANACCCCTTTTGTGAAAGGNGGATAGGCCCGGTTCTGATNTG 2100
Db 2041 CCTCCCCCAANACCCCTTTTGTGAAAGGNGGATAGGCCCGGTTCTGATNTG 2100
QY 2101 GATGCTCCTTAAATNTTGTAGCCATAAACCATTTGCTAGTGTCTTAAATGACAGTT 2160
Db 2101 GATGCTCCTTAAATNTTGTAGCCATAAACCATTTGCTAGTGTCTTAAATGACAGTT 2160
QY 2161 TAGAATAGNGGTTTACTTTTGTATTTTNTTTTGTAGACTGTATTTCTCAATA 2220
Db 2161 TAGAATAGNGGTTTACTTTTGTATTTTNTTTTGTAGACTGTATTTCTCAATA 2220
QY 2221 ATGACATGTTGTTTACTCGAAGTGAAGATAAATACAGAGATTGNAGNAAAAA 2280
Db 2221 ATGACATGTTGTTTACTCGAAGTGAAGATAAATACAGAGATTGNAGNAAAAA 2280
QY 2281 AAAAAAAGGAAAAAAGGAAAAA 2307
Db 2281 AAAAAAAGGAAAAAAGGAAAAA 2307

RESULT 2

ID ABK15494 standard; cDNA; 3039 BP.

AC ABK15494;

XX 08-MAY-2002 (first entry)

DE Wheat starch branching enzyme IIB cDNA from clone wdk2c_pk009.j17.

XX
KW Wheat; starch branching enzyme; starch synthesis; transgenic plant;
KW wdk2c_pk009.j17; antibody; gene mapping; expressed sequence tag;
KW EST; gene; ss.

OS Triticum aestivum.

XX
FH Key Location/Qualifiers
FT CDS 3..2570
FT /*tag= a

FT /product= "Starch branching enzyme IIB"
FT /partial
FT /note= "No start codon shown. The sequence from
FT nucleotides 481-3039 is specifically claimed in
FT claim 3 of the specification and is shown as
FT Seq ID. 1"

XX US2002002713-A1.

PN 03-JAN-2002.

XX 23-FEB-2001; 2001US-0792127.

XX 01-MAR-2000; 2000US-186098P.

XX (ALLE/) ALLEN S M.

XX (BECK/) BECKLES D M.

XX (BUTL/) BUTLER K H.

XX (PEAR/) PEARLSTEIN R W.

PI Allen SM, Beckles DM, Butler KH, Pearlstein RW;

XX WPI; 2002-178959/23.

DR P-PSDB; AAU76219.

XX Novel isolated polypeptide having starch IIB enzyme activity, useful
PT for preparing antibodies to the proteins which are used to detect the
PT polypeptides in situ in cells or in vitro in cell extracts

XX Claim 3; Page 17-18; 27pp; English.

XX This invention relates to the cDNA and protein sequences of a novel
CC wheat starch branching enzyme IIB enzyme. Starch branching enzymes are
CC responsible for the formation of alpha 1-6 linkages in amylopectin in
CC the starch synthesis pathway. The nucleotide sequence of the invention
CC is useful for producing a transgenic plant expressing the starch
CC branching enzyme. The protein sequence is useful for preparing
CC antibodies against starch branching enzyme IIB protein, which are
CC useful for detecting the proteins in situ in cells, or in vitro in cell
CC extracts. The protein is also useful for selecting an isolated
CC polynucleotide that affects the level of expression of a starch
CC branching enzyme IIB protein or enzyme activity in a plant cell. All or
CC substantial portion of the nucleotide sequence can be used as probe for
CC genetic and physical mapping of the genes and can be used as markers for
CC traits linked to those genes. This information is useful in plant
CC breeding in order to develop lines with desired phenotypes. A
CC polynucleotide fragment is useful for isolating cDNAs and genes encoding
CC homologous proteins from the same or other plant species. They are also
CC useful as DNA hybridisation probes or as polymerase chain reaction (PCR)
CC amplification primers. The fragments are also useful for creating
CC transgenic plants and may be useful as restriction fragment length
CC polymorphism markers. Nucleic acid probes derived from the cDNA sequence
CC may also be used for physical mapping or for fluorescence in situ
CC hybridisation (FISH) mapping. The present sequence represents the
CC wheat starch branching enzyme IIB cDNA from clone wdk2c_pk009.j17.

XX Sequence 3039 BP; 836 A; 624 C; 783 G; 796 T; 0 other;

Query Match

91.8%

Score 2118.4; DB 24; Length 3039;

Best Local Similarity 97.2%; Pred. No. 0;

Matches 2191; Conservative 0; Mismatches 54; Indels 8; Gaps 4;

QY 45 TTGGTGTGGGAGATGTTCTTGTCCCAACAATGCAGATGGTTCGCCACCAATTCCTCAGC 104
Db 793 TTGGTGTGGGAGATGTTCTTGTCCCAACAATGCAGATGGTTCGCCACCAATTCCTCAGC 852
QY 105 GCTCAGGGGTGAAGTGAGAAATGATCTCATCTGGGATAAAGGATCAATTCCTGCTT 164
Db 853 GCTCAGGGGTGAAGTGAGAAATGATCTCATCTGGGATAAAGGATCAATTCCTGCTT 912
QY 165 GGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATGGAATGATATATGATC 224
Db 913 GGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATGGAATGATATATGATC 972

[illegible]

<u>RESULT 8</u>	
P93691	
ID	P93691
AC	PRELIMINARY; PRT; 823 AA.
DT	01-MAY-1997 (TREMBlrel. 03, Created)
DT	01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE	1,4-alpha-glucan branching enzyme II precursor (EC 2.4.1.18).
GN	SBE2.
OS	Triticum aestivum (Wheat).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC	Triticeae; Triticum.
OX	NCBI_TaxID=4565;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. FIELDER;
RA	Nair R.B., Baga M., Scoles G.J., Kartha K.K., Chibbar R.N.;
RT	"Isolation, characterization and expression analysis of a starch
RT	branching enzyme II cDNA from wheat.";
RL	Plant Sci. 0:0-0(0).
DR	EMBL; Y11282; CAA72154.1; -.
DR	InterPro; IPR000461; Alpha_amylase.
DR	InterPro; IPR004193; Isoamylase_N.

DR	Pfam: PF00128; alpha-amylase; 1.
DR	Pfam: PF02922; isoamylase_N; 1.
KW	Glycosyltransferase; Signal; Transferase.
FT	SIGNAL 1 54 POTENTIAL.
FT	CHAIN 55 823 1,4-ALPHA-GLUCAN BRANCHING ENZYME II.
SQ	SEQUENCE 823 AA; 92936 MW; 80135FA52CBA4549 CRC64;
<p>Query Match 70.1%; Score 2894; DB 10; Length 823; Best Local Similarity 86.9%; Pred. No. 1.4e-22; Matches 512; Conservative 45; Mismatches 32; Indels 0; Gaps</p>	
QY	14 FGVWEMFLPNADGSPPIPHGSRVKVRMDTPSGIKDISIPAWIKYSVQTPGDIPIYNGIYYD 73
DB	232 YGVWEIFLPNNADGSPAIPHGSRVKIRMDTPSGVKDISISAWIKFSVQAPGEIPFNGIYYD 291
QY	74 PPEEKYVFKHPQKRPKSLRIYETHVGMSSPEPKINTYANFRDEVLPRIKRLGYNAVQI 133
DB	292 PPEEKYVVFQHPQKRPESLRIYESHIGMSSPEPKINSYANFRDEVLPRIKRLGYNAVQI 351
QY	134 MAIQHSYYCGFYHYVTNFFAPSSRFSGPEDLKSLLIDRAHELGLVLMVDVHSHASNNTL 193
DB	352 MAIQHSYYASFGYHYVTNFFAPSSRFSGTPEDLKSLLIDRAHELGLVLMDIVHSHSSNNTL 411
QY	194 DGLNGFDGTDTHYFHGGRGHHWMDSRVFNIGNKEVIRFLLSNARWWLEEYKFDGFRFD 253
DB	412 DGLNGFDGTDTHYFHGGRGHHWMDSRLENYGSWEVLRFLLSNARWWLEEYKFDGFRFD 471
QY	254 GATSMMYTHHGLQVTFGTGSYHEYFGFATDVDVAVYMLMNDLIHGFIYPEAVTIGEDVSGM 313
DB	472 GVTSMMYTHHGLQMTFTGNYGGEYFGFATDVDVAVYMLVNDLIHGLHPDVAVSIGEDVSGM 531
QY	314 PTFALPVQGVGVEDYRLHMAVADKWIELLKGNDEAWEMGNIVHTLTNRRWPEKCVTYAE 373
DB	532 PTFCIPVPDGGVGLDYRLHMAVADKWIELLKQSDSESKMGDIVHTLTNRRWLEKCVTYAE 591
QY	374 SHDQALVGDKTIAFWLMDKMDYDFMALNGPSTPSIDRGIALHKMIRLITMGLGEGYLNF 433
DB	592 SHDQALVGDKTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGEGYLNF 651
QY	434 MGNEFGHPEWIDPPRGPOVLPTGKFTPGNNNSYDKCRRRFDGDAEFLRYHGMQQFDQAM 493
DB	652 MGNEFGHPEWIDPPRGPOQLPTGKVLPCNNNSYDKCRRRFDLGDADFLRYHGMQEFQDAM 711
QY	494 QHLEEKYGMTSDHQYVSRKHEEDKVIIVPEKGDLVFVFNFWHSNSYFDYRVGCLKPGKYK 553
DB	712 QHLEEKYGMTSEHQYVSRKHEEDKVIIFERGDLVFVFNFWHSNSFFDYRVGCSRPGKYK 771
QY	554 VVLDSADAGLFGGFRIHHTAEHTSDCOHDNRPHSFSVYTPSFTCVVYA 602
DB	772 VALDSDDALFGGFSRLDHDVDYFTTEHPHDNRPRSFSVYTPSFTAVVYA 820

```

RESULT 9
Q9ZTB7
ID Q9ZTB7 PRELIMINARY; PRT; 734 AA.
AC Q9ZTB7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Starch branching enzyme IIA (EC 2.4.1.18).
GN SBE1 OR SBEIIA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BOMI;
RX MEDLINE=98404232; PubMed=9733524;
RA Sun C., Sathish P., Ahlandsberg S., Jansson C.;
RT "The two genes encoding starch-branching enzymes II
RT differentially expressed in barley.";
```


Db 2392 GAGCACTTCACCGCGGACTGTTGCGCATGATAATAGGCCATATTCATTCCTCGGTTATACA 2451
 QY 1784 CTTAGCAGAACCTGTGTCTATGCTCCTCAATGAACATA 1822
 Db 2452 CCAAGCAGAACATGTGCTGCTATGCTCCTCAGTGGAGTGA 2490

RESULT 7

AAT69729 standard; DNA; 2665 BP.

XX AAT69729;
 AC AAT69729;
 XX 10-SEP-1997 (first entry)
 DT Plasmid pBE240 insert encoding corn starch branching enzyme IIb.
 XX Starch branching enzyme IIb; SBEIIb; corn; maize; antisense;
 DE amylopectin; transgenic plant; pBE240; ss.
 XX Zea mays.

Key Location/Qualifiers
 CDS 79..2478
 /*tag= a

WO9722703-A2.

25-JUN-1997.

XX 12-DEC-1996; 95WO-US19678.
 XX 20-DEC-1995; 95US-0009113.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Broglie KE, Hubbard NL, Klein TM;
 PI WPI: 1997-341694/31.
 XX P-PSDB; AAW19212.

Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff

Example 1; Page 50-53; 92pp; English.

A cDNA insert (AAT69729) in plasmid clone pBE240 comprises a 2.7 kb EcoRI-XhoI fragment isolated from a corn cDNA library. It includes an open reading frame encoding starch branching enzyme IIb (SBEIIb) (AAW19212). The insert was used as a starting point in the assembly of DNA constructs (see also AAT69730, AAT69736-37) designed to achieve suppression of SBEIIb expression in transgenic corn plants, and thereby to produce novel starches that have properties beneficial in food and industrial applications.

Sequence 2665 BP; 700 A; 525 C; 705 G; 735 T; 0 other;

Query Match 59.8%; Score 1380.6; DB 18; Length 2665;
 Best Local Similarity 86.0%; Pred. No. 9.2e-305;
 Matches 1530; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 44 TTTGGTGTGGGAGATGTTCTTGGCAACAATGCAGATGGTTGCGCCACCAATTCCTCAC 103
 Db 700 TTTGGTGTGGGAAATTTTCTGCTAAACAATGCAGATGGTTGCGCCACCAATTCCTCAT 759
 QY 104 GGCTCAGGGTGAAGGTGAGAAATGGAATGCTCCATCTGGGATAAAGGATTCATTCCTGCT 163
 Db 760 GGATCTCGTGAAGGTGAGAAATGGAATGCTCCATCAGGATAAAGGATTCATTCAGCC 819
 164 TGGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCAATGGAATATATATGAT 223

Db 820 TGGATCAAGTACTCAGTGCAGGCCCCAGGAGAAATACCATATGATGGGATTTATATGAT 879
 QY 224 CCTCCGGAAGAGAGAAAGTATGTATTCAGCATCCTCAACCTAAACGACCAAAATCATG 283
 Db 880 CCTCCTGAAGAGGTAAAGTATGTGTTCAGGCATCGCAACCTAAACGACCAAAATCATG 939
 QY 284 CGGATATATGAACACACATGTTGGCATGAGTAGCCCGGAAACCAAAAGATCAACACATATGCA 343
 Db 940 CGGATATATGAACACACATGTCGGAATGAGTAGCCCGGAAACCAAAAGATCAACACATATGTA 999
 QY 344 AACTTCAGGGATGAGGTGCTTCCCAAGAAATTAAGAGACTTGGATACAATGCAGTGCAATA 403
 Db 1000 AACTTTAGGGATGAAGTCTCTCCCAAGAAATTAAGAGACTTGGATACAATGCAGTGCAATA 1059
 QY 404 ATGGCAATCCAGAGCACTCATATTTATGGAAGCTTTGGGTACCATGTTACCAATTTCTTT 463
 Db 1060 ATGGCAATCCAGAGCACTCATATTTATGGAAGCTTTGGGTACCATGTTACCAATTTCTTT 1119
 QY 464 GCACCAAGTAGCCGTTTGGGTCCCGAGAAAGATTTAAATCTTTGATTGATAGAGCTCAC 523
 Db 1120 GCGCCAAGTAGTCTGTTTGGTACCCCGAGAAAGATTTGAAGTCTTTGATTGATAGAGCACAT 1179
 QY 524 GAGCTTGGCTTGTGCTCCTCATGGATGTTGTTTACAGTCAACGCTCAAAATATACCTTG 583
 Db 1180 GAGCTTGGTGTGCTGTTTCTCATGGATGTTGTTTACAGTCAACGCTCAAAATATACCTTG 1239
 QY 584 GACGGGTGAATGCTTGTGATGGCAGCATACACATTTACATTTTACAGTGGTCCAGCTGGC 643
 Db 1240 GATGGGTGAATGCTTGTGATGGTACAGATACACATTTACATTTTACAGTGGTCCAGCTGGC 1299
 QY 644 CATCACTGGATGCGGATTCCTCATGGATGTTGTTTACAGTCAACGCTCAAAATATACCTTG 703
 Db 1300 CATCACTGGATGCGGATTCCTCATGGATGTTGTTTACAGTCAACGCTCAAAATATACCTTG 1359
 QY 704 CTACTTTCCAATGCAAGATGGTGGCTAGAGGAGTATAAGTTGATGGTTCCTCGATTCGAT 763
 Db 1360 CTCTCTCCAATGCTAGATGGTGGCTAGAGGAGTATAAGTTGATGGTTCCTCGATTCGAT 1419
 QY 764 GCGCGACCTCCATGATGTATACCCATCATGGATGTTTACAGTCAACGCTCAAAATATACCTTG 823
 Db 1420 GGTGTGACCTCCATGATGTATACCTCATGGATGTTTACAGTCAACGCTCAAAATATACCTTG 1479
 QY 824 CATGAATATTTTGGCTTTCCTCATGGATGTTGTTTACAGTCAACGCTCAAAATATACCTTG 883
 Db 1480 AATGAGTATTTTGGCTTTCCTCATGGATGTTGTTTACAGTCAACGCTCAAAATATACCTTG 1539
 QY 884 GATCTAATTCATGGGTTTATCCTGAGCCGTAACATATCGGTGAAGATGTTAGTGAATG 943
 Db 1540 GATCTAATTCATGGGTTTATCCTGAGCCGTAACATATCGGTGAAGATGTTAGTGAATG 1599
 QY 944 CCTACATTTGCCCTTCTGTTTCAAGTGGTGGGTTGTTGTTGACTATCGCTTACATATG 1003
 Db 1600 CCTACATTTGCCCTTCTGTTTCAAGTGGTGGGTTGTTGTTGACTATCGGTGATCATATG 1659
 QY 1004 GCTGTTGCCGACAAATGGATTGAACCTTCTCAAGGAAACGATGAAGCTTGGGAGATGGGT 1063
 Db 1660 GCTGTTGCCGACAAATGGATTGAACCTTCTCAAGGAAACGATGAAGCTTGGGAGATGGGT 1719
 QY 1064 AATATTGTGCACACACTAACAACACAGAGGTGGCCGAAAGTGTGTTACTTATGCTGAA 1123
 Db 1720 GATATTGTGCACACACTAACAACACAGAGGTGGTTAGAGAGTGTGTAACCTTATGCTGAA 1779
 QY 1124 AGTCACGATCAAGCACTGGTTGGGAGACAAGACTATTGTCATCTCTGTTGATGGCAAGGAT 1183
 Db 1780 AGTCATGATCAAGCACTGGTTGGGAGACAAGACTATTGTCATCTCTGTTGATGGCAAGGAT 1839
 QY 1184 ATGTATGATTTTCATGGCTCTGAACGAGCACTTCGACACCTTACTATTGATCGTGAATAGCA 1243
 Db 1840 ATGTATGATTTTCATGGCTCTGAACGAGCACTTCGACACCTTACTATTGATCGTGAATAGCA 1899
 QY 1244 CTGCATAAATGATTTAGACTTATCAACATGGGTTTAGGAGAGAGGTTTATCTTAACCTT 1303
 Db 1900 TTACATAAGATGATTAGACTTATCAACATGGGTTTAGGAGAGAGGCTTATCTTAATTTTC 1959

QY 1304 ATGGGAATGAGTTCGGGCATCCTGAATGGATAGACTTTTCAAGAGGCCCCACAGTACTT 1363
|||||
Db 1960 ATGGGAATGAGTTTGGACATCCTGAATGGATAGATTTTCAAGAGGTCGGCAACACTT 2019
|||||
QY 1364 CCAACTGGTAAGTTTCATCCAGGAACAACAACAGTTTACGACAAATGCCGTGGAAGATT 1423
|||||
Db 2020 CCAAGTGGTAAGTTTATTCAGGGAATAACAACAGTTTACAAATGTCTGCGAAGATT 2079
|||||
QY 1424 GACCAGGTGATGCAGAAATTTCTAGGTATCATGGTATGACAGCAGTTTGTATCAGGCGATG 1483
|||||
Db 2080 GACCTGGTGATGCAGACTATCTTAGGTATCATGGTATGCAAGAGTTTGTATCAGGCAATG 2139
|||||
QY 1484 CAGCATCTTGAGGAAAAAATATGGCTTTATGACATCAGACCAACAGTACGTATCTCGGAAA 1543
|||||
Db 2140 CAACATCTTGAGCAAAAAATATGAATTCATGACATCTGATCACCAGTATATTTCCCGGAAA 2199
|||||
QY 1544 CATGAGGAAGATAAGGTGATCGTGTCTTGAAGAAAGGGGACTTGGTATTTGTGTTCAACTTC 1603
|||||
Db 2200 CATGAGGAGATAAGGTGATCTGTCTCGAAAAGGGAGATTGGTATTTGTGTTCAACTTC 2259
|||||
Y 1604 CACTGAGTAATAGCTATTTTCGACTACCGGGTTGGCTGTGTTTAAAGCCCTGGGAGTACAAG 1663
|||||
Db 2260 CACTGCAACAACAGCTATTTGACTACCGTATTTGGTTGTCGAAAGCCCTGGGGTGTATAAG 2319
|||||
QY 1664 GTTCTCTTAGACTCAGACCGCGGACTCTTTGGTGGATTGGTAGGATCCATCAGACTGCA 1723
|||||
Db 2320 GTGGTCTTGACTCCGACCGTGGACTATTTGGTGGATTAGCAGGATCCATCAGCGAGCC 2379
|||||
QY 1724 GACCACCTTCACTTCTGACTGCCAACATGACAACAGGCCCATTCGTTCTCAGTGACACT 1783
|||||
Db 2380 GAGCACTTCACCGCCGACTGTTCGCATGATAATAGGSCATATTCATCCTCGGTTATACA 2439
|||||
QY 1784 CCTAGCAGAACCTGTGTGTCTATGCTCCCAATGAATAA 1822
|||||
Db 2440 CCAAGCAGAACATGTGTCTATGCTCCAGTGGAGTGA 2478
|||||

RESULT 8
AAV05639
ID AAV05639 standard; cDNA to mRNA; 3015 BP.
XX
AC AAV05639;
XX
DT 01-MAY-1998 (first entry)
XX
DE Rice type IV starch branching enzyme cDNA.
XX
KW Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
X
OS Oryza sativa.
XX
FH Key Location/Qualifiers
CDS 129..2654
FT /*tag= a
FT sig_peptide 129..287
FT /*tag= b
FT mat_peptide 288..2651
FT /*tag= c
FT /product= type_IV_starch_branching_enzyme
XX
PN JP10004970-A.
XX
PD 13-JAN-1998.
XX
PF 24-JUN-1996; 96JP-0162983.
XX
PR 24-JUN-1996; 96JP-0162983.
XX
PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA (MITK) MITSUI TOATSU CHEN INC.
XX
DR WPI; 1998-133625/13.

P-PSDB; AAW41763.
XX Rice starch branching enzyme gene - synthesises amylopectin to yield high quality starch
PS Claim 4; Pages 5-8; 13pp; Japanese.
XX The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch is improved by the use of the protein.
XX Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;
SQ
Query Match 56.8%; Score 1310.4; DB 19; Length 3015;
Best Local Similarity 83.8%; Pred. No. 9.5e-289;
Matches 1482; Conservative 0; Mismatches 286; Indels 0; Gaps 0;
QY 44 TTTGGTGTGGGAGATGTTCTTGCCAAAACAATGCAGATGGTTCGCCACCAATTCCTCAC 103
|||||
Db 873 TATGGTGTGGGAGATTTCCTTGCCTAAACAATGCTGATGGATCCCTGCTATTCTCAT 932
|||||
QY 104 GGCTACCGGGTGAAGGTGAGAAATGATATCTCCATCTGGGATAAAGGATTCAATTCTCTGCT 163
|||||
Db 933 GGCTACCGTGAAGATTTCGGATGATACACCATCTGGCGTAAAGGATTCAATTCTCTGCC 992
|||||
QY 164 TGGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATACAATGGAATATATATGAT 223
|||||
Db 993 TGGATTAAGTTTGTGTGCAGGCTCCAGGTGAATACCGTACAACGGTATATATATGAT 1052
|||||
QY 224 CCTCCGGAAGAGGAGAAGTATGTATTTCAAGCATCTCAACCTAAACGACCAAAATCATTTG 283
|||||
Db 1053 CCACCTGAAGAAGAAAAATATGTATTTCCAACATCTCAACCTAAACGACCAAAATTCGCTG 1112
|||||
QY 284 CGGATATATGAACACATGTTGGCATGAGTAGCCCGGAGAACCAACCAAGATCAACACATATGCA 343
|||||
Db 1113 CGGATATATGAATCACATATTTGAATGAGTAGCCCGGAACCGGAAGATATAACACATATGCT 1172
|||||
QY 344 AACTTCAGGGATGAGGTGCTTCCAAAGAATTTAAAGACTTGGATACAATGCAGTCAAAATA 403
|||||
Db 1173 AATTTAGGGATGAGGTGCTACCAAGAATTTAAAGAGTTCGGGTACAATGCTGTACAGATA 1232
|||||
QY 404 ATGCAATCCAGGAGCACATCATACTATGGAAGCTTTGGGTACCATGTTACCAATTTCTTT 463
|||||
Db 1233 ATGCAATCCAGGAGCACATCTTATACGCAAGCTTTGGGTATCATGTTACTACTTCTTT 1292
|||||
QY 464 GCACCAAGTAGCCGTTTTGGTCCCCCAGAGAATTTAAATCTTTGATTGATAGAGCTCAC 523
|||||
Db 1293 GCACCAAGTAGCCGTTTCGGAACCCCAAGAGACTTGAATCTCTGATTGATAAAGCTCAC 1352
|||||
QY 524 GAGCTTGGCTTGGTTGCTCCTCATGGATGTTGTTTCAAGTCACGCGTCAAAATACCTTG 583
|||||
Db 1353 GAGCTTGGTTTGTCTGACTATGGATATTGTTTCAAGTCATGATCAAAACAATACCTTG 1412
|||||
QY 584 GACGGTTGAATGGTTTGTGATGGCAGGATACACATTAATCTTCCATGGCGTTTACCGGGC 643
|||||
Db 1413 GATGGTTTGAATGGTTTGTGATGGTACTGATACACATTAATCTTCCATGGTGACCGGGGT 1472
|||||
QY 644 CATCACTGGATGTGGGATTTCCCGTGTGTTTAACTATGGAATAAGGAAGTTATAAGGTTT 703
|||||
Db 1473 CATCACTGGATGTGGGATTTCTCGCTGTTCACACTATGGGAGTTGGGAAGTTTAAAGATAT 1532
|||||
QY 704 CTACTTTCCAATGCAAGATGGTGGCTAGAGGAGTATAAGTTTGTATGGTTTCCGATTCGAT 763
|||||
Db 1533 TTAAGTGTGAATGCAAGGTGGTGGCTTGAAGATAACAAGTTTGTATGGTTTTCGATTTGAT 1592
|||||
QY 764 GCGCGACCTCCATGATGATATACCCATCATGGAATACAAGTAACTTTACAGGAAGCTAC 823
|||||
Db 1593 GGGGTGACCTCCATGATGATATCTACTCATCATGTTTACAGGTGGCAATTTACTGGCACTAT 1652
|||||
QY 824 CATGAATATTTTGGCTTTGCCACTGATGATAGATCGGTCGTTTACTTACTGATGATGAAT 883
|||||
Db 1653 GGCGAATATTTTGGATTTGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1712
|||||

Db 1982 ATGTATGATTTTCATGGCTCTGGATAGGCTTCAACTCCTCGCATTTGATCGTGGCATAGCA 2041
QY 1244 CTGCATAAAATGATTAGACTTATACAAATGGGTTTAGGAGGAGAGGGTTATCTTAACCTTT 1303
Db 2042 TTACATAAAATGATCAGGCTTGTCCACCATGGGTTTAGTGTGAAGGCTATCTTAACCTTC 2101
QY 1304 ATGGGAAATGAGTTCGGGCATCCTGATGATAGACTTTTCAAGAGAGGCCACACAGTACTT 1363
Db 2102 ATGGGAAATGAGTTCGGGCATCCTGATGATAGACTTTTCAAGAGAGGCCACACAGTACTT 2161
QY 1364 CCAACTGGTAAAGTTCATCCAGGAACAACAACAGATTACGACAAATGCCGTCGAAGATTT 1423
Db 2162 CCAACCGGCAAGTTCCTCCCTGGAAATAACAATAGTTATGATAAATGCCGCCGATAGATT 2221
QY 1424 GACCAAGGTGATGACAGAAATTTCTAGGTATCATGTTATGACAGCAGTTTGTATCAGGCGATG 1483
Db 2222 GATCTTGGAGATGACAGATTTCTTCTAGATATCATGTTATGCAAGAGTTCGATCAGGCAATG 2281
QY 1484 CAGCATCTTGAGGAAATATGGCTTTATGACATCAGACACAGTACGTATCTCGGAAA 1543
Db 2282 CAGCATCTTGAGGAAATATGGCTTTATGACATCAGACACAGTATGTTTTCACGGAAA 2341
QY 1544 CATGAGGAAGATGAGGTGATCGTGTGTTGAAAAGGGGACTGGTATTTGTGTTCAACTTC 1603
Db 2342 CATGAGGAAGATGAGGTGATCATCTCGAAAGAGGAGATTGGTATTTGTTTCAACTTC 2401
QY 1604 CACTGGAGTAATAGTATTTTCGACTACCGGGTGTGGCTGTTTAAAGCCTGGGAAGTACAAG 1663
Db 2402 CACTGGAGTAATAGTATTTTTCGACTACCGGGTGTGGCTGTTTAAAGCCTGGGAAGTACAAG 2461
QY 1664 GTTGTCTTAGACTCAGACCGCGGACTCTTTGGTGGATTTGGTAGGATCCATCAGTACTGCA 1723
Db 2462 GTGGCCTTAGACTCCGACGATGCACCTTTGGTGGATTCAGCAGGCTTGATCATGATGTC 2521
QY 1724 GAGCACTTCACCTTCTGACTGCCAACATGACAAACAGGCCCCCATTCGTTCTCAGTGTACACT 1783
Db 2522 GACTACTTCACACCGGAACATCCGCGATGACAAACAGGCCCCGCTCTTTCTCGGTTGATCACT 2581
QY 1784 CCTAGCAGAACCTGTGTGTCTATGCTTCCCAATGAACATAACAGCA 1828
Db 2582 CCGAGCAGAACCTGGGTGCTGTATGCGCTTACAGAGTAAAGAACCA 2626

RESULT 11
TASBA2
LOCUS TASBA2 2970 bp mRNA linear PLN 27-FEB-1997
DEFINITION T.aestivum mRNA for starch branching enzyme II.
ACCESSION Y11282
VERSION Y11282.1 GI:1885343
KEYWORDS 1,4-alpha-glucan branching enzyme; sbe2 gene; starch branching enzyme II.
SOURCE Triticum aestivum.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 2970)
AUTHORS Nair,R.B., Baga,M., Scoles,G.J., Kartha,K.K. and Chibbar,R.N.
TITLE Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
JOURNAL Plant Sci.
REFERENCE 2 (bases 1 to 2970)
AUTHORS Chibbar,R.N.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, CANADA
FEATURES
Source
1. .2970
/organism="Triticum aestivum"
/cultivar="Fielder"
/db_xref="taxon:4565"
/clone="PRN33"

/dev_stage="kernels 12 days post anthesis"
151. .2948
/gene="sbe2"
151. .2622
/gene="sbe2"
/EC_number="2.4.1.18"
/codon_start=1
/product="1,4-alpha-glucan branching enzyme II"
/protein_id="CAA72154.1"
/db_xref="GI:1885344"
/db_xref="SPTREMBL:P93691"
/translation="MATFAVSGATLGVARPAGAGGGLPRSGSERRGGVDLPSLLLRK
KDSRAVLSRAASPGKVLVPDGSDDLSPAQPEELQIPEDIEEQTAENVMTGGTAEK
LESSEPTQIVETITDGVTKVKELVVEKPRVVPKPGDQKIYEIDPTLDFRSHLD
YRYSEYRIRAAIDQHEGGLFAPSRGKLGFTSRSAEGTYREWAPGAHSAALVGFDFN
WNPNDATMRDDYGVWEIFLPNNADGSPAIPHGSRVKIRMDTPSGKDSISAWIKFS
VQAPGEIPFNGIYYDPEEEKYVFQHPQKRPESLRVIESHIGMSSPEPKINSYANFR
DEVLPRIKRLGYNVQIMAIQEHSYASFGYHVTNFPAPSSRFPTPEDLSLIDRAHE
LGLLVMDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPRGHMMWDSRLFNYSWEVLR
FLLSNARWLEEKFDGFRDGVTSMMYTHHGLQMTFTGNYGEYFGFATDVAVVYLM
LVNDLIHGLHPDAVISIGEDVSGMPTFCIPVDPGGVGLDYRLHMAVADKWIELKQSDP
SWKMGDIVHTLTNRWLEKCVTAESHDAQLVGDKTIAFWLMDKMDYDFMALDRPSTP
RIDRGIALHKMIRLVMTGLGEGYLNFMNEFGHPWDPRGPQTLPTGKVLPGNNN
SYDKRRRFDLGDADFLRYHGMQEFDAQMHLEEKYFMTSEHQYVSRKHEEDKVIIF
ERGDLVFVFNHWSNFFDYRVGCSRPGKYKVALDSDDALFEGGFSRLDHDVDYFTTEH
PHDNRPSFSVYTPSRTAVVYALTE"
151. .312
/gene="sbe2"
313. .2619
/gene="sbe2"
/product="1,4-alpha-glucan branching enzyme II"
/EC_number="2.4.1.18"
2879. .2884
/gene="sbe2"
2930. .2935
/gene="sbe2"
2948
/gene="sbe2"
BASE COUNT 782 a 640 c 775 g 773 t
ORIGIN
Query Match 56.6%; Score 1306.6; DB 8; Length 2970;
Best Local Similarity 83.2%; Pred. No. 1.3e-307;
Matches 1486; Conservative 0; Mismatches 299; Indels 0; Gaps 0;
QY 44 TTTGGTGTGGGAGATGTTCTGCCAAACATGACAGATGGTTGCCACCAATTCCTCAC 103
Db 844 TATGGTGTGGGAGATTTCTCCCTCAACAATGCTGATGGATCCCGAGTATTCCTCAT 903
QY 104 GGCTACGGGTGAAGGTGAGATGGATCTCCATCTGGGATAAAGGATCAATTCCTGCT 163
Db 904 GGCTACGGTGAAGATACGGATGGATCTCCATCTGGTGTGAAGGATCAATTCCTGCT 963
QY 164 TGGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATCAATGGAATATATATGAT 223
Db 964 TGGATCAAGTCTCTGTGCAGGCTCCAGGTGAATACCATTCATGGCATATATATGAT 1023
QY 224 CTTCCCGAAGAGGAGATATGTTTCAAGCATCTCAACCTAAACGACCAAAATCATG 283
Db 1024 CCACCTGAAGAGGAGATATGTTTCCAAACATCTCAACCTAAACGACCAAGTCACTG 1083
QY 284 CGGATATATGAACACATGTTGGCATGAGTAGCCCGGAACCAAGATCAACACATATGCA 343
Db 1084 AGGATTTATGAATCACACATGGAATGAGCAGCCAGAACCGAAGATAAATTCATATGCT 1143
QY 344 AACTTCAGGATGAGGTGCTTCCAAAGAAATTAAGAACTTGGATACATGCAAGATA 403
Db 1144 AATTTAGGATGAGGTGCTTCCAAAGAAATTAAGAACTTGGATACATGCAAGATA 1203
QY 404 ATGGCAATCCAGGAGGACTCATACTATGGAAGCTTTGGGTACCATGTTACCAATTTCTTT 463
Db 1204 ATGGCAATCCAGGAGGACTCATACTATGGAAGCTTTGGGTACCATGTTACCAATTTCTTT 1263

QY 464 GCACCAAGTAGCCGTTTGGGTCCCCAGAAGATTAAAAATCTTTGATTGATAGAGCTCAC 523
|||||
Db 1264 GCACCAAGTAGCCGTTTGGAACTCCAGAGGACTTAAATCCCTGATGATAGACACAT 1323
|||||
QY 524 GAGCTTGGCTTGGTTCCTCATGGATGTTGTTTCACAGTCAAGCGTCAAAATAATACCTTG 583
|||||
Db 1324 GAGCTTGGTTCCTTCTTATGGATATGTTTCATAGTCAATTCATCAAAATAATACCCCT 1383
|||||
QY 584 GACGGGTTGAATGGTTTGTATGGCAGCGATACACATTACTTCCATGGCGGTTTCACGGGCG 643
|||||
Db 1384 GACGGCTTGAATGGTTTCGATGGCACTGATACACATTACTTCCACGGTGGTCCACGTCGC 1443
|||||
QY 644 CATCACTGGATGGGATTCCTCGTGTGTTAACTATGGGAATAAGGAAGTTTATAAGGTTT 703
|||||
Db 1444 CATCATTTGGATGGGATTCCTCGTCTATTCAACTATGGGAGTTGGGAAGTATTGAGATTC 1503
|||||
QY 704 CTACTTTCCAATGCAAGATGGTGGCTAGAGGAGTATAAGTTTGATGGTTTCCGATTCGAT 763
|||||
Db 1504 TTACTGTCAACCCGAGATGGTGGCTTGAAGAATAATAAGTTTGATGGATTCGATTTGAT 1563
|||||
QY 764 GCGCGGACCTCCATGATGTATACCCATCATGGATTACAAGTAACCTTTACAGGAAGCTAC 823
|||||
Db 1564 GGGGTGACCTCCATGATGTATACTCACCATGGATTACAAATGACATTTACTGGGAACATAT 1623
|||||
QY 824 CATGAATATTTGGCTTTGCCACTGATGTAGATCGGGTCGGTTTACTTGTGCTGATGAAT 883
|||||
Db 1624 GCGGAGTATTTGGATTTGCTACTGATGTGATGCGGTAGTTTACTTGTGCTGGTCAAC 1683
|||||
QY 884 GATCTAATTCATGGGTTTATCCTGAAGCGGTAACCTATCGGTGAAGATGTTAGTGAATG 943
|||||
Db 1684 GATCTAATTCATGGACTTCATCCTGATGCTGTATCCATTGGTGAAGATGTCAGTGAATG 1743
|||||
QY 944 CCTACATTTGCCCTTCTGTTCAAGTTGGTGGGTTGGTTTGGTACTATCGCTTACATATG 1003
|||||
Db 1744 CCCACATTTTGACCTCCCTGTTCCAGATGGTGGTGTGGTTTGGACTATCGCTTGATATG 1803
|||||
QY 1004 GCTGTTCCGCAAAATGATGTTGAACCTTCTCAAGGAAACGATGACCTTTGGGAGATGGGT 1063
|||||
Db 1804 GCTGTAGCAGATAAATGGATTGAACCTCTCAAGCAAAAGTGACGGAATCTTGGAAAATGGGT 1863
|||||
QY 1064 AATATTGTGCACACACTAACAAACAGAGAGGTGGCGGGAAGTGTGTACTTATGCTGAA 1123
|||||
Db 1864 GATATTGTGCACACCCCTAACAAATAGAAGTGGCTTGAGAAAGTGTAACTTATGCGAA 1923
|||||
QY 1124 AGTCACGATCAAGCACTGGTTGGAGACAAAGACTATTGCATTCCTGGTTGATGGCAAGGAT 1183
|||||
Db 1924 AGTCATGATCAAGCACTAGTTGGTGACAAGACTATTGCATTCCTGGTTGATGGATAAGGAT 1983
|||||
QY 1184 ATGTATGATTTCATGGCTCTGAACGGACCTTCGACACCTAGTATTGATCGTGAATAGCA 1243
|||||
Db 1984 ATGTATGATTTTCATGGCTCTGGATAGGCTTCAACTCCTCGCAATTGATCGTGGCATAGCA 2043
|||||
QY 1244 CTGCATAAAATGATTAGACTTATCACAATGGGTTTAGGAGGAGAGGGTTATCTTAACTTT 1303
|||||
Db 2044 TTACATAAAATGATCAGGCTTGTCAACCATGGGTTTAGGTGGTGAAGCTATCTTAACTTC 2103
|||||
QY 1304 ATGGGAAATGAGTTCGGGCATCCTGATGGATAGACTTTCCAAGAGGCCCCACAAAGTACTT 1363
|||||
Db 2104 ATGGGAAATGAGTTTGGGCATCCTGATGGATAGATAGATTTTCCAAGAGAGTCCGCAAACTCTT 2163
|||||
QY 1364 CCAACTGGTAAGTTCATCCCAGGAAACAACAAGATTTACGACAATATGCCGTGCAAGATTT 1423
|||||
Db 2164 CCAACCGGCAAGTCTCCCTGGAAATAACAATAGTTTATGATAAATGCCGCCGTAGATTT 2223
|||||
QY 1424 GACCAGGTTGATGCAGAAATTTCTTAGGTATCATGGTATGCAGCAGTTTGTATCAGGCGATG 1483
|||||
Db 2224 GATCTTGGAGATGCAGATTTTCTTAGATATCATGTTGATGCAAGAGTTCGATCAGGCAATG 2283
|||||
QY 1484 CAGCATCTTGAGGAAAAATATGGCTTTTATGACATCAGACCACCACCTACGTATCTCGGAAA 1543
|||||
Db 2284 CAGCATCTTGAGGAAAAATATGGGTTTATGACATCTGAGCACCCAGTATGTTTTCACGGAAA 2343
|||||
QY 1544 CATGAGGAAGATAAGGTGATCGTGTTTGAAAAAAGGGGACTTGGTATTGTTGTCTCAACTTC 1603
|||||

Db 2344 CATGAGGAAGATAAGGTGATCATCTTCGAAAGAGGAGATTGGTATTGTTTCAACTTC 2403
|||||
QY 1604 CACTGGAGTAATAGCTATTTCGACTACCGGCTGGCTGTTTAAAGCCTGGGAAGTACAAG 1663
|||||
Db 2404 CACTGGAGCAATAGCTTTTTCGACTACCGTGTGGTGTTCAGGCTGGGAAGTACAAG 2463
|||||
QY 1664 GTTGTCTTAGACTCAGACGCCGACTCTTTGGTGGATTGGTAGGATCCATCACAATGCA 1723
|||||
Db 2464 GTGGCTTAGACTCCGACGATGCATCTTTGGTGGATTTCAGCAGGCTGATCATGATGC 2523
|||||
QY 1724 GAGCACTTCACTTCTGACTGCCAATGACAAACAGGCCCCCATTCGTTCTCAGTGTACACT 1783
|||||
Db 2524 GACTACTTCACAAACCGAACAATCCGCATGACAAACAGGCGCGCTCTTCTCGGTGTACACT 2583
|||||
QY 1784 CCTAGCAGAACTGTGTTGTCTATGCTCCAATGAACATAAACAGCA 1828
|||||
Db 2584 CCGAGCAGAACTGCGTGTGTATGCCCTTACAGAGTAAGAACCA 2628
|||||
RESULT 12
AF064560
LOCUS
DEFINITION
AF064560
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS
translation="MAEVNMTGGAAGAAKLESEPTQGIABITDGTGKVKELVVGKPK
QVVPKPGDGQKIYEIDPTLKDFRSHLDYRSEYKRIIRAIDQHEGGLGVSRGYEKL
FTRSAKITYREWAPGAHSAALVGFDFNNPNADTMRDDYGVWEIFLPNNADGSPAI
PHGSVKIRMDTPSGVKDSISAWIKFSVQAPGEIPFNGIYDPPPEEKYVFQHPQPKR
PESLRIYESHIGMSSPEKINSYANFRDEVLPRIKRLGYNVQVIMAIQHSYVYASFGY
HVTNFPAPSSRFCTPEDKSLIDRAHELGLLVLMWDIVHSHSSNNTLDGLNGFDGTDTH
YFHGGPRGHMMWDSRLFNYSWEVLRFLLSNARWMLFEYKFGDFRFDGVTSMYTHH
GLQMTFTGNYGEYFGFATDVAVVYLMVNDLIHGLYDAVSIIGEDVSGMPTFCIPVP
DGGVGFDRYRLHMAVADKWIELLKQSDSWKMGDIIVHTLTNRRLWLEKCVTYAESHDQAL
VGDKTIAFWLMDKMDYDFMALDRPSTPRIDRGIALHKMIRLVMTGLGEGYLNFMGNE
FGHFEWIDFPRGPQTLPTGKVLPGNNNSYDCRRRLDGLDADFLRYRGMQEFQAMQH
LEEKYGMTSEHQYVSRKHEEDKVIIFERGLVFFVFNHWSNSKDYRVGCSKPGKYK
VALDSDDALFGGFSRLDHDVDYFTTEHPHNRPRSFVSVTPSRTAVVYALTE"